AMENDMENTS TO THE SPECIFICATION

Please insert the following Tables 1, 2, 3, 4, 5 and 6 after paragraph [0112] and before the Claims.

Table 1
Number and Frequency (%) of ACTN3 Genotypes and Frequency
(%) of ACTN3 Alleles in Controls and Elite Sprint/Power and
Endurance Athletes

	No. (%	Allele Frequency (%)			
GROUP (n)	RR	RX	·XX	R	X
Malor					
Controls (134)	40 (30)	73 (54)	21 (16)	57	43
Sprint (72)	38 (53)	28 (39)	6 (8)	72	28
Endurance (122)	34 (28)	63 (52)	25 (20)	54	46
Pemale:	• •	• •	1		• -
Controls (292)	88 (30)	147 (50)	57 (20)	<i>\$</i> 5	45
Sprint (35)	15 (43)	20 (57)	0 (0)	71	29
Endurance (72)	26 (36)	25 (35)	21 (29)	53	47
Total:	• •		1 1		•••
Controls (436)	130 (30)	226 (52)	80 (18)	56	44
Sprint (107)	53 (50)	48 (45)	6 (6)	72	28
Endurance (194)	60 (31)	88 (45)	46 (24)	54	46

Strength	Sport	ID	Sport Institute	Total Number	577RR (%)	577RX (%)	577XX (%)
Endurance	Rower	RT492	AIS	64	22	28	14
		-			(34.4%)	(43.8%)	(21.8%)
		RT556					
Endurance	Triathloner	RT977	AIS	13	3	8	2
		•			(23.1%)	(61.5%)	(15.4%)
· · · · · · · · · · · · · · · · · · ·		RT989				•	•
Endurance	Cyclist	RT990	AIS	9	4	2	3
		-	•	j	(44.4%)	(22.2%	(33.3%)
		RT998				•	` .
Endurance	Track	KN246	AIS	22	7	7	8
-	Cyclist	•			(31.8%)	(31.8%)	(36.4%)
		KN275					
Endurance	Marathon	KN310	AIS	1	0	0	1
Endurance	All above		AIS	108	36	45	27
					(33,3%)	(41.7%)	(25.0%)
Sprint	Swimmer	RT901	AIS	45	17	25	3
		-			(37.8%)	(55.6%)	(6.6%)
•		RT1018		<u> </u>			
Sprint .	Track	KN246	AIS	8	. 4	3	· 1
	Cyclist	-			(50.0%)	(37.5%)	(12.5%)
		KN275					
Sprint	Athletics	KN276	AIS	30	16	13	i
		-			(53,3%)	(43.3%)	(3.3%)
		KN309					
Sprint	All above	<u> </u>	AIS	83	37	41	5
					(44.6%)	(49.4%)	(6.0%)
Africa Zulu		, <u>"</u>		88	69	18	1
, , , , , , , , , , , , , , , , , , ,	i.				(78.4%)	(20.5%)	(1.1%)
Australian				152	46	· 78	28
Caucasian	,				(30.0%)	(52,0%)	(18%)
Control						~-·-·	

Table 3 SNPs identified in the ACTN3 gene to date NCBI SNP CLUSTER ID

rs2229456 rs2229455 rs2229454 rs2228325 rs1126675 тв7949754 rs7924602 rs5792393 rs4990284 rs4990283 rs4013815 rs3937320 тв3837428 тв3814736 rs3814735 rs3782080 rs2511217 rs2511216 rs2509559 rs2509558 rs2305537 rs2305534 rs2290463 rs2275998 rs2096583 rs2000939

rs1815739

rs1791690 rs1671064 rs679228

rs678397

rs677488

rs647476

rs647029

rs618838

rs607736

rs597626

rs544021

rs540874

rs538330

rs531490

га509556

rs490998

rs13897

rs4576

rs1189338

rs1201433

rs640213

rs3737525

rs3178740

rs3180065

rs3180064

rs3180063

rs3867132

rs608504

rs610293

rs3825065

TABLE 4. Symbols, full names, and cytogenic location of nuclear and mitochondrial genes of the 2002 Human Gene Map for Performance and Health-Related Fitness Phenotypes.

Gene or Locus Name Location

AB

ACADVL Acyl coenzyme A dehydrogenase, very long chain 17p13-p11

ACE Angiotensin I converting enzyme 17q23

ADRA2A Alpha-2A-adrenergic receptor 10q24-q26

ADRBI Adrenergic, beta-1-, receptor 10q24-q26

ADRB2 Beta-2-adrenergic receptor 5g31-g32

ADRB3 Beta-3-adrenergic receptor 8p12-p11.2

AGT Angiotensinogen 1q42-q43

ANG Angiogenin, ribonuclease, RNase A family, 5 14q11.1-q11.2

APOE Apolipoprotein E 19q13.2

ATPIA2 ATPase, Na_/K_ transporting, alpha-2 polypeptide 1q21-q23

ATP1B1 ATPase, Na_/K_ transporting, beta 1 polypeptide 1q22-q25

BDKRB2 Bradykinin receptor B2 14q32.1-q32.2

CDEFG

CASO2 Calsequestrin 2 (cardiac muscle) 1p13.3-p11

CFTR Cystic fibrosis transmembrane conductance regulator, ATP-binding cassette (sub-

family C, member 7) 7q31.2

CKM Creatine kinase, muscle 19q13.2-q13.3

CNTF Ciliary neurotrophic factor 11q12.2

CPT2 Carnitine palmitoyltransferase 2 1p32

COLIAI Collagen, type I, alpha 1 17q21.3-q22.1

EDNI Endothelin 1 6p24.1

ENO3 Enolase 3, (beta, muscle) 17pter-p11

FABP2 Fatty acid binding protein 2 4q28-q31

FGA Pibrinogen, A alpha polypeptide 4q28

FGB Fibrinogen, B beta polypeptide 4q28

GDF8 (MSTN) Growth differentiation factor 8 (myostatin) 2q32.2

GNB3 Guanine nucleotide binding protein (G protein), beta polypeptide 3 12p13

HIKLM

HLA-A Major histocompatibility complex, class I, A 6p21.3

HP Haptoglobin 16q22.1

IGFI Insulin-like growth factor I 12q22-q23

IGF2 Insulin-like growth factor 2 11p15.5

IL-6 Interleukin-6

KCNQ1 K_voltage-gated channel, KQT-like subfamily, member 1 11p15.5

LDHA Lactate dehydrogenase A 11p15.4

LPL Lipoprotein lipase 8p22

MTCO1 Cytochrome c oxidase I mtDNA 5904-7445

MTCO3 Cytochrome c oxidase III mtDNA 9207-9990

MTCYB Cytochrome b mtDNA 14747-15887

MTNDI NADH dehydrogenase 1 mtDNA 3307-4262

MTND4 NADH dehydrogenase 4 mtDNA 10760-12137

MTND5 NADH dehydrogenase 5 mtDNA 12337-14148

MTTE Transfer RNA, mitochondrial, glutamic acid mtDNA 14674–14742

MTTI Transfer RNA, mitochondrial, isoleucine mtDNA 4263-4331

MTTK Transfer RNA, mitochondrial, lysine mtDNA 8295-8364

MTTL1 Transfer RNA, mitochondrial, leucine 1 (UUR) mtDNA 3230-3304

MTTL2 Transfer RNA, mitochondrial, leucine 2 (CUN) mtDNA 12266-12336

MTTM Transfer RNA, mitochondrial, methionine mtDNA 4402-4469

MTTT Transfer RNA, mitochondrial, threonine mtDNA 15888-15953

MTTY Transfer RNA, mitochondrial, tyrosine mtDNA 5826-5891

MyHC myosin Heavy-chain

NOPQRSTUV

NOS3 Nitric oxide synthase 3 (endothelial cell) 7q36

NPY Neuropeptide Y 7p15.1

PAII Plasminogen activator inhibitor 1 7q21.3-q22

PFKM Phosphofructokinase, muscle 12q13.3

PGAM2 Phosphoglycerate mutase 2 (muscle) 7p13-p12

PGK1 Phosphoglycerate kinase 1 Xq13

PHKA1 Phosphorylase kinase, alpha 1 (muscle) Xq12-q13

PONI Paraoxonase 1 7q21.3

PPARA Peroxisome proliferative activated receptor, alpha 22q13.31

PPARG Peroxisome proliferative activated receptor, gamma 3p25

PYGM Phosphorylase, glycogen, muscle 11q12-q13.2

RYR2 Ryanodine receptor 2 (cardiac) 1q42.1-q43

SGCA Sarcoglycan, alpha (50kDa dystrophin-associated glycoprotein) 17q21

S100A1 S100 calcium binding protein A1 1q21

SUR Sulfonylurea receptor 11p15.1

TGFB1 Transforming growth factor beta 1 19q13.2

UCP2 Uncoupling protein 2 11q13

UCP3 Uncoupling protein 3 11q13

VDR Vitamin D (1,25-dihydroxyvitamin D3) receptor 12q12-q14

The gene symbols, names and cytogenetic locations are from the Locus Link web site available from the National Center for Biotechnology Information (NCBI). For mitochondrial DNA, locations are from the human mitochondrial genome data base.

TABLE 5. Endurance phenotypes and case-control studies (DNA polymorphisms).

		Athle	tes			Cont	rols
Gene	Location	N	Sports	Freq.	N	Freq.	P
ADRA2A	10q24-q26	140	Endurance	6.7/6.7: 0.77	141	6.7/6.7: 0.62	0.037
				6.7/6.3: 0.21		6.7/6.3: 0.34	
				6.3/6.3: 0.02		6.3/6.3: 0.04	
				6.7: 0.88		6.7: 0.8	0.011
				6.3: 0.12		6.3: 0.2	
ACE	17q23	64	Endurance	II: 0.30	118	П: 0.18	0.03
				ID: 0.55		ID: 0.51	
				DD: 0.16		DD: 0.32	
				I: 0.57		I: 0.43	0.02
				D: 0.43		D: 0.57	
		79	Running	I: 0.57	Ref.	I: 0.49	0.039
		95	Managata	D: 0.43	Pop.	D: 0.51	A AA
		25	Mountain- ecring	NA	Ref.	NA	0.02
			** **		Pop.		0.003
		60	Elite athelets (cycling,	II: 0.25	Ref.	П: 0.16	0.0009
			running, handball)				
			•	ID: 0.58	Pop.	ID: 0.45	
				DD: 0.17	-	DD: 0.39	
				I: 0.54		I: 0.38	
				D: 0.46		D; 0.62	
		56	Elite swimmers	П: 0.15	1248	II: 0.24	0.004
	· 1		(subsample				
			of 103 swimmers)				
			•	ID: 0.39		ID: 0.49	
				DD: 0.46		DD: 0.27	
				I: 0.34		I: 0.48	
				D: 0.66		D: 0.52	

Reference: Perusse et al. 2003 "The human gene map for performance and health-related fitness phenotypes: the 2002 update" Med. Sci. Sports Exerc. 35: 1248-1264.

TABLE 6. Genotype and allelic frequencies of ACTN3 577R/X alleles in human populations.

Ethnic group	No. of chromosomes	No. of genotypes		Relative allele
		RX	XX	frequency of 577X
Asian	56	14	7	0.5±0.07
Javanese	96	28	12	0.54 <u>+</u> 0.05
Native American	14	2	2	0.43 <u>+</u> 0.14
Asia/Americas	166	44	21	0.52 <u>+</u> 0.04
Hispanic	64	16	5	0.41 <u>+</u> 0.06
White	214	47	21	0.42 <u>+</u> 0.03
Europe	278	63	26	0.41 <u>+</u> 0.03
Aboriginal	174	33	9	0.29±0.03
Australian				
PNG Highlander	78	16	6	0.36 <u>+</u> 0.05
Australasia	252	49	15	0.31 <u>+</u> 0.03
African American	90	12	6	0.27±0.05
African Bantu	156	14	1	0.10 <u>+</u> 0.05
Africa	246	56	7	0.16 <u>+</u> 0.05
Unknown	152	50	11	0.47
Total	1094	232	80	